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BMT/8/17 Add.
ORIGINAL: English
DATE: September 18, 2003

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS

GENEVA

WORKING GROUP ON BIOCHEMICAL AND MOLECULAR TECHNIQUES AND DNA-PROFILING IN PARTICULAR

Eighth Session
Tsukuba, Japan, September 3 to 5, 2003

ADDENDUM TO DOCUMENT BMT/8/17

STATISTICAL ASPECTS OF ESSENTIAL DERIVATION

Presentation prepared by experts from the Netherlands and the United Kingdom

Statistical Aspects of Essential Derivation

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Presentation based on work-packages from the EU funded FP 5 project

Molecular and other Markers for Establishing Essential Derivation (EDV) in Crop Plants.
(MMEDV)

Rose, Maize and Barley

MMEDV: Barley

Material Studied.

a). 46 Barley Varieties from the Finnish National List and UK Recommended List

b). Kustaa x Wanubet Back-cross family

c). Other situations where potential EDV's could occur

This presentation will focus on the first 2 of these

MMEDV: Barley

Markers [not all markers applied to all data types (a), (b) and (c)].

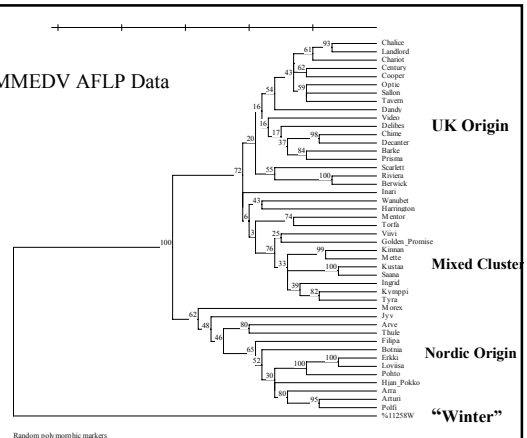
1. ***AFLP (both mapped and un-mapped)***
2. ***S-SAP***
3. ***IRAP***
4. ***REMAP***

AFLP	**Amplified Fragment Length Polymorphisms**
S-SAP	**Sequence-Specific Amplified Polymorphism**
IRAP	**Inter-Retrotransposon Amplified Polymorphism**
REMAP	**Retrotransposon-Microsatellite Amplified Polymorphism**

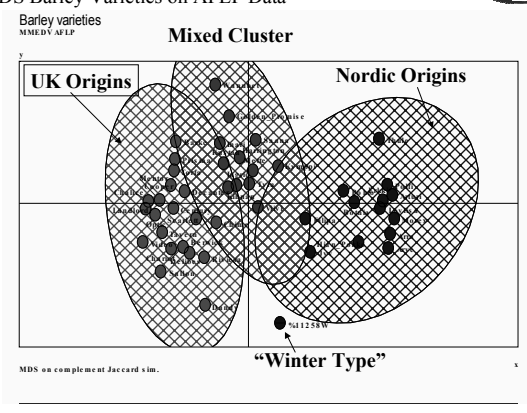
In addition "phenotypic" data [morphology] was available for most data types (b) and (c).

This presentation will major on the first of these but refer to other marker data as well

Barley MMEDV AFLP Data



MDS Barley Varieties on AFLP Data



PCO Plot (Axis 1 v 2 ~ 31.6% VAF). Barley BARE CGC Retrotransposon

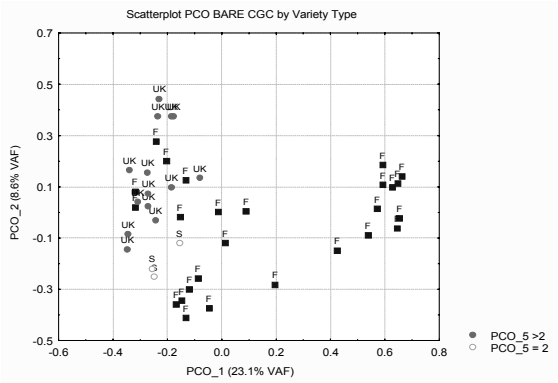
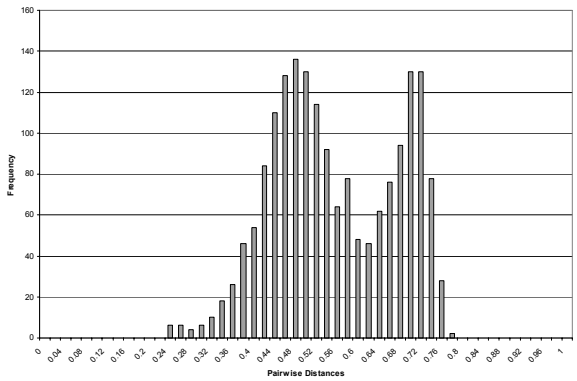


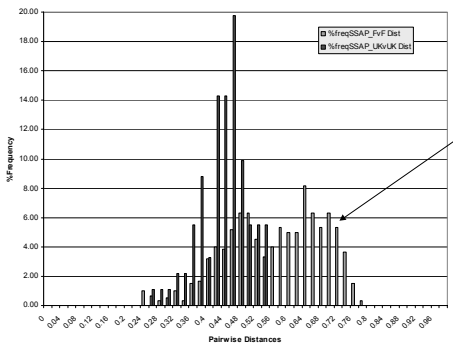
Table 1. Quartile pair-wise distances barley varieties partitioned into Finnish and UK material

Quartiles	Finland and UK	Finland	UK
Q0	**0.2279**	0.2279	0.2427
Q1	**0.4542**	0.4677	0.3971
Q2	**0.5273**	0.5692	0.4390
Q3	**0.6620**	0.6520	0.4626
Q4	**0.7524**	0.7617	0.5344
Q3-Q1	**0.2078**	0.1843	0.0655

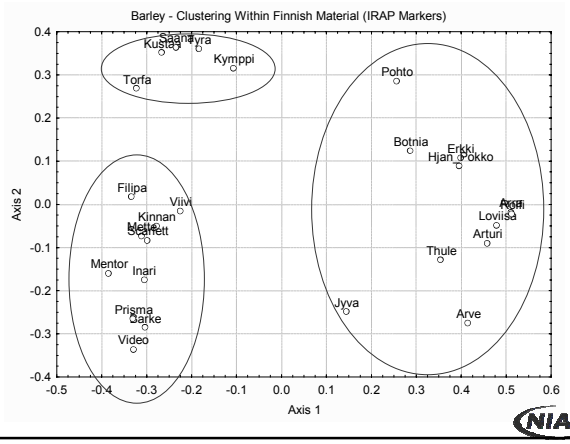
Distribution of Pair-wise Distances SSAP Markers for "National List" Variety Set (Material from both Finland and UK).



Distribution of Pair-wise Distances SSAP Markers for "National List" Variety Set Within Finnish [Blue] and Within UK [Red].

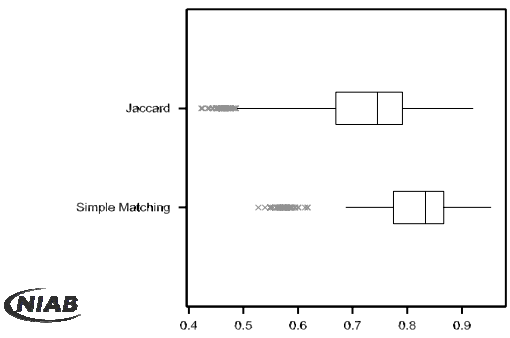


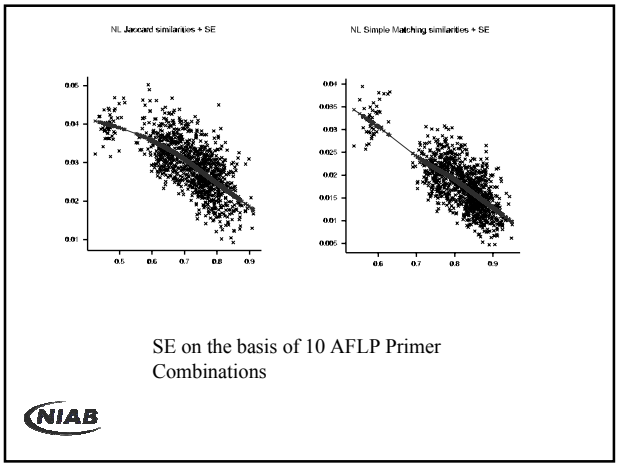
Note degree of residual multi-modality even within Finnish material ~ linked to type/end-use and other factors



Listing of the barley variety with the highest similarity in terms of large pair-wise similarity coefficients (figures under 'Jaccard' column) using AFLP data (se = standard error)

q	Va	Vb	Var a	Var b	Jaccard	se
0.9994	20	12	Saana	Kustaa	0.9209	0.0159
0.9984	14	6	Loviisa	Erkki	0.9179	0.0166
0.9975	37	31	Landlord	Chalice	0.9141	0.0122
0.9965	43	39	Berwick	Riviera	0.9078	0.0294
0.9955	35	33	Decanter	Chime	0.9021	0.0198
0.9946	37	32	Landlord	Chariot	0.8991	0.0172
0.9936	16	11	Mette	Kinnan	0.8966	0.0164
0.9926	19	2	Polfi	Arturi	0.8910	0.0281
0.9917	17	6	Pohto	Erkki	0.8889	0.0164
0.9907	24	13	Tyra	Kymppi	0.8840	0.0309
0.9897	28	13	Ingrid	Kymppi	0.8810	0.0180
0.9888	42	37	Cooper	Landlord	0.8804	0.0150
0.9878	40	31	Sallon	Chalice	0.8790	0.0177





SE on the basis of 10 AFLP Primer Combinations

Precision of the distance/similarity coefficients is estimateable and is decreasing with increasing similarity levels.

Absolute precision will vary depending on marker systems and numbers of primer combinations (bands).

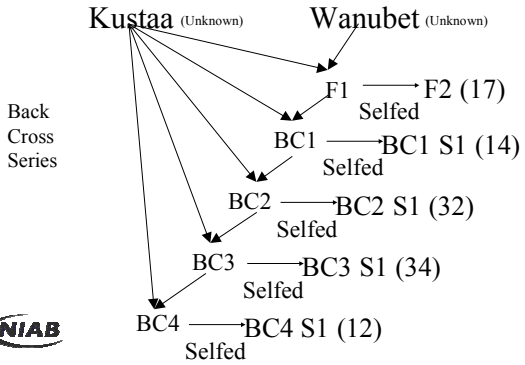
In barley, with 10 AFLP PC's , 95% CI are circa 0.08 and LSD 0.056 for Jaccard's and 0.04(95% CI) and 0.28 (LSD) for Simple Matching.

Barley Back-cross Family

(Kustaa x Wanubet)

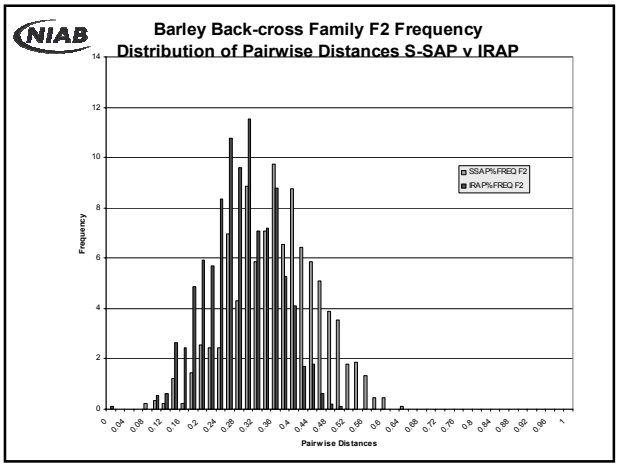
Kustaa x Wanubet Back-cross Family

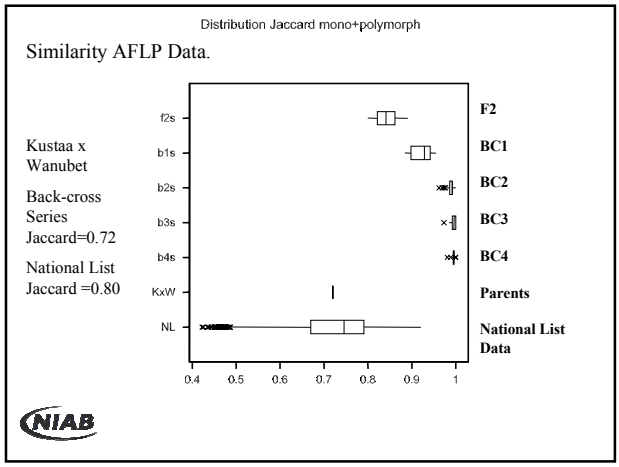
(Number of individuals assessed by phenotype and DNA)

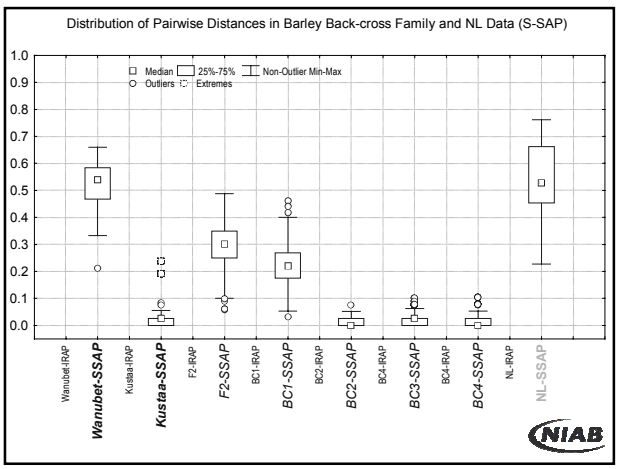


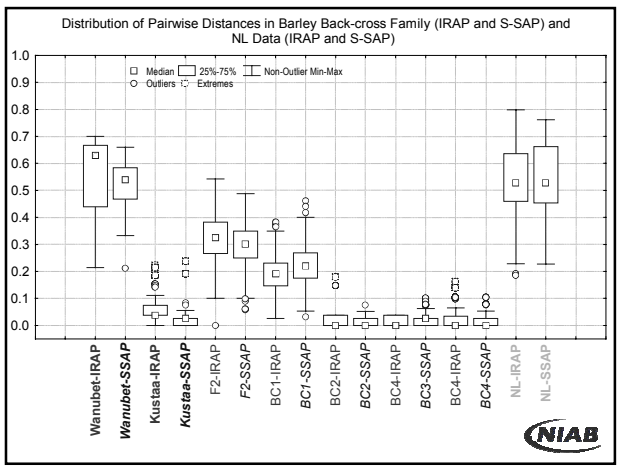
Good Agreement between S-SAP and IRAP/REMAP markers.

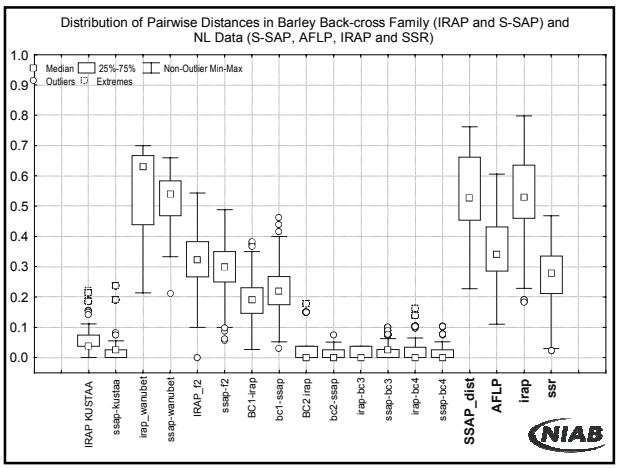
Standard quartile statistics and plots of the distribution of pair-wise distances; illustrate this.











Barley back-cross Family Descriptive Statistics for Pair-wise Distances Based on S-SAP and IRAP Marker Systems.

Descriptive Statistics	S-SAP F2	IRAP F2	S-SAP BC1	IRAP BC1	S-SAP BC2	IRAP BC2	S-SAP BC3	IRAP BC3	S-SAP BC4	IRAP BC4
Q0	0.077	0.000	0.039	0.026	0.000	0.000	0.000	0.000	0.000	0.000
Q25	0.281	0.225	0.261	0.146	0.000	0.000	0.000	0.000	0.000	0.000
Q50	0.353	0.278	0.333	0.191	0.000	0.000	0.053	0.000	0.000	0.000
Q75	0.419	0.333	0.393	0.231	0.053	0.029	0.053	0.029	0.053	0.031
Q100	0.640	0.488	0.667	0.381	0.150	0.135	0.191	0.029	0.191	0.147
Q3-Q1	**0.138**	**0.108**	**0.132**	**0.085**	**0.053**	**0.029**	**0.053**	**0.029**	**0.053**	**0.031**

All marker systems showed increased similarity/ reduced distance between BC1 and BC2 with little further change in BC3, BC4

Conclusions

This project has clearly demonstrated that molecular markers of various kinds provide an objective and efficient means of determining the relatedness between genotypes of different crops and hence have an important role in helping to establish suitable thresholds for potential ED situations.

In addition,markers also provide evidence that could help resolve instances of ED.

Given that there is a relationship between the DUS testing of newly bred varieties and ED, in that an EDV has to sufficiently D, U and S and thus exceed the "minimum distance" criterion for the establishment of D, the results from the project are also of relevance to future approaches to DUS testing *per se*.

Any EDV framework needs to be evaluated on a crop by crop basis and then based on 'grouped material'. This was also seen in Maize (Flint v Dent), Barley in this project (MMEDV) and in lettuce (ISF funded work).

Statistical tools exist and can be applied to specific crops and marker systems (a number appear to be appropriate) in the context of assessing an EDV framework.

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